

SEQUENCE LISTING

<110> Chamson, Pierre - Metzger, Daniel

<120> Transgenic mouse for targeted recombination mediated by modified Cre-ER

<130> D18961

<150> FR 00 12 570
<151> 2000-10-03

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1788)

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atc ccc ctg gag cgg ccc ctg ggc gag gtg tac ctg gac agc agc aag	144
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ccc gcc gtg tac aac tac ccc gag ggc gcc tac gag ttc aac gcc	192
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gcg gcc gcc aac gcg cag gtc tac ggt cag acc ggc ctc ccc tac	240
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ggc ccc ggg tct gag gct gcg ggc ttc ggc tac aac ggc ctg ggg ggt	288
Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly	
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ttc ccc cca ctc aac agc gtg tct ccg agc ccg ctg atg cta ctg cac	336
Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His	
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ccg ccg cag ctg tcg cct ttc ctg cag ccc cac ggc cag cag gtg	384
Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val	
115 120 125	

ccc tac tac ctg gag aac gag ccc agc ggc tac acg gtg cgc gag gcc	432
Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala	
130 135 140	

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Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly	
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Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met	
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gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat gct	576
Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala	
180 185 190	
tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc ttc	624
Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe	
195 200 205	
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Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr	
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aac cag tgc acc att gat aaa aac agg agg aag agc tgc cag gcc tgc	720
Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys	
225 230 235 240	
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Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg	
245 250 255	
aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga gat	816
Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp	
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Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala	
275 280 285	
gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag aac	912
Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn	
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Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro	
325 330 335	
tcc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac agg	1056
Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg	
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Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu	
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 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
 465 470 475 480
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 Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
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 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
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 <213> Homo sapiens

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Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
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Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr
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 85 90 95

Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
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Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly
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Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr
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Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg
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Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
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 275 280 285

Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
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Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
 305 310 315 320

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 Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
 340 345 350
 Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
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 Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
 370 375 380
 Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly
 385 390 395 400
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 Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
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 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Phe Val Cys Leu
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 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
 450 455 460
 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
 465 470 475 480
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 485 490 495
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 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
 515 520 525
 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
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 <212> DNA
 <213> Artificial sequence

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<221> CDS

<222> (1)...(1983)

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gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg	96
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg	
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gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt	144
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val	
35 40 45	

tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt	192
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ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg	240
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65 70 75 80	

cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac	288
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atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct	336
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala	
100 105 110	

gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt	384
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly	
115 120 125	

gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag	432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln	
130 135 140	

gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat	480
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145 150 155 160	

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165 170 175	

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Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg	
180 185 190	

atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt	624
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly	
195 200 205	

gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg	672
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 225 230 235 240

cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta 768
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 245 250 255

tca act cgc gcc ctg gaa ggg att ttc gaa gca act cat cga ttg att 816
 Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Tle
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tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga 864
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
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cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt 912
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tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att 960
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gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg 1008
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335

cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga 1056
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
 340 345 350

gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag 1104
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 385 390 395 400

ccc ttc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac 1248
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
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agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca ggc ttt 1296
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
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450

455

460

ggg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga 1440
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aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca 1488
 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
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agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg 1632
 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
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gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg 1680
 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
 545 550 555 560

acc ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc 1728
 Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
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tcc cac atc agg cac atg agt aac aaa aya atg gag cat ctg tac agc 1776
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atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag atg 1824
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ctg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc 1872
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gtg gag gag acg gac caa aag tat tac atc acg ggg gag gca gag ggt ttc 1920
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<213> Artificial sequence

<223> Chimeric sequence Homosapiens-Bacteriophage P1

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Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
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Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
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Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
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Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
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Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
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Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
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Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
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Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
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Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
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His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
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Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
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Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
 340 345 350
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
 355 360 365
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
 370 375 380
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
 385 390 395 400
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
 405 410 415
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
 420 425 430
 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
 435 440 445
 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
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 Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly
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 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
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 500 505 510
 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser
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 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
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 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
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 Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
 565 570 575
 Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser
 580 585 590
 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met
 595 600 605
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 610 615 620
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Pro Ala Thr Val
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<221> CDS
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<223> Chimeric sequence Homosapiens-Bacteriophage P1

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Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Ser Val
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Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
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Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
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Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct 336
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt 384
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag 432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat 480
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

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 165 170 175

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 Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190 195

atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt
 Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205 210

gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg
 Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
 210 215 220 225

att tcc gtc tct ggt gta gct gat gat ccg aat aac tac ctg ttt tgc
 Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240

cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta
 Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
 245 250 255 260

tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att
 Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270 275

tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285 290

cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300 305

tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320

gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335 340

ccg ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
 340 345 350 355

gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
 355 360 365 370

aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
 370 375 380 385

ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
 385 390 395 400

ccc ttc agt gaa gct tcg atg ggc tta ctg acc aac ctg gca gac
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
 405 410 415 420

405

410

415

agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca ggc ttt 1296
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
 420 425 430

gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg 1344
 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
 435 440 445

cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca 1392
 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
 450 455 460

gtg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga 1440
 Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly
 465 470 475 480

aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca 1488
 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
 485 490 495

tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc 1536
 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
 500 505 510

ctc aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc 1584
 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser
 515 520 525

agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg 1632
 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
 530 535 540

gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg 1680
 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
 545 550 555 560

acc ctg cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc 1728
 Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
 565 570 575

tcc cac atc egg dac atg agt aac aaa ggc atg gag cat ctg tac agc 1776
 Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser
 580 585 590

atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag gcg 1824
 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala
 595 600 605

gcg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc 1872
 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620

gtg gag gag acg gac caa aag tat tac atc acg ggg gag gca gag ggt ttc 1920
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

tcc cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc 1968
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655

cct gcc aca gct tga
 Pro Ala Thr Ala
 660

1983

<210> 6

<211> 660

<212> PRT

<213> Artificial sequence

<223> Chimeric sequence Homosapiens-Bacteriophage Pl

<400> 6

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
 210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
 245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
250 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
325 330 335

Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
340 345 350

Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
355 360 365

Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
370 375 380

Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
385 390 395 400

Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
405 410 415

Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
420 425 430

Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
435 440 445

Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
450 455 460

Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly
465 470 475 480

Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
485 490 495

Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
500 505 510

Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser
515 520 525

Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
530 535 540

Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
545 550 555 560

Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
565 570 575

Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser

580

585

590

Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala
 595 600 605

Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620

Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655

Pro Ala Thr Ala
 660

<210> 7

<211> 1983

<212> DNA

<213> Artificial sequence

<220>

<221> CDS

<222> (1)...(1983)

<220>

<223> Chimeric sequence Homosapiens-Bacteriophage Φ1

<400> 7

atg tcc aat tta ctg acc gta cac caa aat ttg cct gca tta ccg gtc 48
 Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15

gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg 96
 Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30

gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144
 Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

tgc cgg tcc tgg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt 192
 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg 240
 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288
 Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct 336
 Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt 384

Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly	
115							120					125				
gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag															432	
Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln	
130							135				140					
gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat															480	
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn	
145							150			155			160			
ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa															528	
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu	
165							170			175						
att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga															576	
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg	
180							185			190						
atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt															624	
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	
195							200			205						
gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg															672	
Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	
210							215			220						
att tcc gtc tct ggt gta gct gat gat ccg aat aac tac ctg ttt tgc															720	
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	
225							230			235			240			
cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta															768	
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	
245							250			255						
tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att															816	
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
260							265			270						
tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga															864	
Tyr	Gly	Ala	Lys	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly		
275							280			285						
cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt															912	
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
290							295			300						
tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att															960	
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
305							310			315			320			
gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg															1008	
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
325							330			335						
cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga															1056	
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Ile	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	
340							345			350						
gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag															1104	
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys		

355

360

365

aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu 370	375	380	1152	
ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg 385	390	395	400	1200
ccc ttc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp 405	410	415	1248	
agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca ggc ttt Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe 420	425	430	1296	
gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp 435	440	445	1344	
cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro 450	455	460	1392	
ggg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly 465	470	475	480	1440
aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr 485	490	495	1488	
tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys 500	505	510	1536	
ctc aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser 515	520	525	1584	
agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu 530	535	540	1632	
gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu 545	550	555	560	1680
acc ctg cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc Thr Leu Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu 565	570	575	1728	
tcc cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser 580	585	590	1776	
atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag gcg Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala 595	600	605	1824	

gcg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc 1872
 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620

gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca 1920
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc 1968
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655

cct gcc aca gct tga 1983
 Pro Ala Thr Ala
 660

<210> 8

<211> 660

<212> PRT

<213> Artificial sequence

<223> Chimeric sequence Homosapiens-Bacteriophage P1

<400> 8

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205
 Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
 210 215 220
 Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240
 Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
 245 250 255
 Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
 340 345 350
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
 355 360 365
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
 370 375 380
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
 385 390 395 400
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
 405 410 415
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
 420 425 430
 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
 435 440 445
 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
 450 455 460
 Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly
 465 470 475 480
 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
 485 490 495
 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
 500 505 510
 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser

515

520

525

Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
 530 535 540

Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
 545 550 555 560

Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
 565 570 575

Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser
 580 585 590

Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala
 595 600 605

Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620

Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655

Pro Ala Thr Ala
 660

<210> 9
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 9
 tccttcacca agcacatctg

20

<210> 10
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 10
 tgcagccctc acaactgtat

20

<210> 11
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 11
 caacctgcac ttgtcactta g

21

<210> 12
 <211> 20
 <212> DNA

22

<213> Homo sapiens

<400> 12

atgtttcata gttggatata

20

<210> 13

<211> 37

<212> DNA

<213> Mus musculus

<400> 13

atacgcggcc gggaaattcca gcaggaatca ggttagct

37

<210> 14

<211> 37

<212> DNA

<213> Mus musculus

<400> 14

atagcgcggg cgtgcagca caggagggtg ctatgag

37